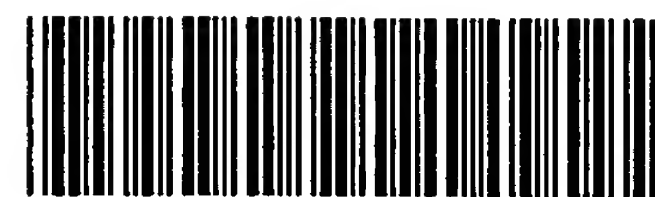# RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/074,694_

Source: _1FW16_

Date Processed by STIC: _07-05-2005_

ENTERED

IFW16

RAW SEQUENCE LISTING   DATE: 07/05/2005
PATENT APPLICATION: **US/10/074,694**   TIME: 14:27:54

Input Set : **A:\10276-017002.TXT**
Output Set: **N:\CRF4\07052005\J074694.raw**

```
 4 <110> APPLICANT: Kahn, C. Ronald
 5        Zhu, Jianhua
 7 <120> TITLE OF INVENTION: MODULATING THE RAD-NM23 INTERACTION
10 <130> FILE REFERENCE: 10276-017002
12 <140> CURRENT APPLICATION NUMBER: US 10/074,694
13 <141> CURRENT FILING DATE: 2002-02-12
15 <150> PRIOR APPLICATION NUMBER: US 09/053,967
16 <151> PRIOR FILING DATE: 1998-04-02
18 <160> NUMBER OF SEQ ID NOS: 5
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 308
24 <212> TYPE: PRT
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
28 Met Thr Leu Asn Gly Gly Gly Ser Gly Ala Gly Gly Ser Arg Gly Gly
29 1               5                   10                  15
30 Gly Gln Glu Arg Glu Arg Arg Arg Gly Ser Thr Pro Trp Gly Pro Ala
31              20                  25                  30
32 Pro Pro Leu His Arg Arg Ser Met Pro Val Asp Glu Arg Asp Leu Gln
33              35                  40                  45
34 Ala Ala Leu Thr Pro Gly Ala Leu Thr Ala Ala Ala Ala Gly Thr Gly
35      50                  55                  60
36 Thr Gln Gly Pro Arg Leu Asp Trp Pro Glu Asp Ser Glu Asp Ser Leu
37 65                  70                  75                  80
38 Ser Ser Gly Gly Ser Asp Ser Asp Glu Ser Val Tyr Lys Val Leu Leu
39                  85                  90                  95
40 Leu Gly Ala Pro Gly Val Gly Lys Ser Ala Leu Ala Arg Ile Phe Gly
41              100                 105                 110
42 Gly Val Glu Asp Gly Pro Glu Ala Glu Ala Ala Gly His Thr Tyr Asp
43              115                 120                 125
44 Arg Ser Ile Val Val Asp Gly Glu Glu Ala Ser Leu Met Val Tyr Asp
45      130                 135                 140
46 Ile Trp Glu Gln Asp Gly Gly Arg Trp Leu Pro Gly His Cys Met Ala
47 145                 150                 155                 160
48 Met Gly Asp Ala Tyr Val Ile Val Tyr Ser Val Thr Asp Lys Gly Ser
49                  165                 170                 175
50 Phe Glu Lys Ala Ser Glu Leu Arg Val Gln Leu Arg Arg Ala Arg Gln
51              180                 185                 190
52 Thr Asp Asp Val Pro Ile Ile Leu Val Gly Asn Lys Ser Asp Leu Val
53              195                 200                 205
54 Arg Ser Arg Glu Val Ser Val Asp Glu Gly Arg Ala Cys Ala Val Val
55      210                 215                 220
```

```
56 Phe Asp Cys Lys Phe Ile Glu Thr Ser Ala Ala Leu His His Asn Val
57 225             230             235             240
58 Gln Ala Leu Phe Glu Gly Val Val Arg Gln Ile Arg Leu Arg Arg Asp
59             245             250             255
60 Ser Lys Glu Ala Asn Ala Arg Arg Gln Ala Gly Thr Arg Arg Arg Glu
61             260             265             270
62 Ser Leu Gly Lys Lys Ala Lys Arg Phe Leu Gly Arg Ile Val Ala Arg
63             275             280             285
64 Asn Ser Arg Lys Met Ala Phe Arg Ala Lys Ser Lys Ser Cys His Asp
65     290             295             300
66 Leu Ser Val Leu
67 305
70 <210> SEQ ID NO: 2
71 <211> LENGTH: 664
72 <212> TYPE: DNA
73 <213> ORGANISM: Mus musculus
75 <220> FEATURE:
76 <221> NAME/KEY: CDS
77 <222> LOCATION: (1)...(498)
79 <400> SEQUENCE: 2
80 cag tcg cag ccg gcg gta aag cct tgt cat ctg aag ggg acc atg gcc   48
81 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
82 1               5               10              15
84 aac agt gag cgt acc ttc att gcc atc aag cct gat ggg gtc cag cgg   96
85 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
86              20              25              30
88 ggg ctg gtg ggc gag atc atc aag cgg ttc gag cag aag ggg ttc cgc  144
89 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
90         35              40              45
92 ctt gtt ggt ctg aag ttt ctg cag gct tca gag gac ctt ctc aag gag  192
93 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
94     50              55              60
96 cac tac act gac ctg aag gac cgc ccc ttc ttt act ggc ctg gtg aaa  240
97 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
98 65              70              75              80
100 tac atg cac tca gga cca gtg gtt gct atg gtc tgg gag ggt ctg aat  288
101 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
102             85              90              95
104 gtg gtg aag aca ggc cgc gtg atg ctt gga gag acc aac ccc gca gac  336
105 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
106             100             105             110
108 tct aag cct ggg acc ata cga gga gac ttc tgc att caa gtt ggc agg  384
109 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
110             115             120             125
112 aac atc att cat ggc agc gat tct gta aag agc gca gag aag gag atc  432
113 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
114     130             135             140
116 agc ttg tgg ttt cag cct gag gag ctg gtg gag tac aag agc tgt gcg  480
117 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
```

```
118 145                 150              155              160
120 cag aac tgg atc tat gag tgataggacg gtgccggttt tctacctgct        528
121 Gln Asn Trp Ile Tyr Glu
122                 165
124 tactcttgtt ctcacaggca ggggaccagc aaccctagat atttctggaa cttctttgac 588
125 ctggaaggaa cctttgggag ccgtgactcc ctgtgcagtg ttacgtgcca ctgttagatt 648
126 aaagtgttta atctgt                                                 664
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 166
130 <212> TYPE: PRT
131 <213> ORGANISM: Mus musculus
133 <400> SEQUENCE: 3
134 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
135 1               5               10              15
136 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
137             20              25              30
138 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
139         35              40              45
140 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
141     50              55              60
142 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
143 65              70              75              80
144 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
145             85              90              95
146 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
147             100             105             110
148 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
149         115             120             125
150 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
151     130             135             140
152 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
153 145             150             155             160
154 Gln Asn Trp Ile Tyr Glu
155             165
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 670
160 <212> TYPE: DNA
161 <213> ORGANISM: Homo sapiens
163 <220> FEATURE:
164 <221> NAME/KEY: CDS
165 <222> LOCATION: (73)...(528)
167 <400> SEQUENCE: 4
168 cggccacgag gcggaatccc ttctgctctc ccagcgcagc gccgccgccc ggcccctcca 60
169 gcttcccgga cc atg gcc aac ctg gag cgc acc ttc atc gcc atc aag ccg 111
170              Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro
171               1               5               10
173 gac ggc gtg cag cgc ggc ctg gtg ggc gag atc atc aag cgc ttc gag   159
174 Asp Gly Val Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu
175     15              20              25
```

```
177 cag aag gga ttc cgc ctc gtg gcc atg aag ttc ctc cgg gcc tct gaa   207
178 Gln Lys Gly Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu
179  30               35               40               45
181 gaa cac ctg aag cag cac tac att gac ctg aaa gac cga cca ttc ttc   255
182 Glu His Leu Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe
183              50               55               60
185 cct ggg ctg gtg aag tac atg aac tca ggg ccg gtt gtg gcc atg gtc   303
186 Pro Gly Leu Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val
187              65               70               75
189 tgg gag ggg ctg aac gtg gtg aag aca ggc cga gtg atg ctt ggg gag   351
190 Trp Glu Gly Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu
191          80               85               90
193 acc aat cca gca gat tca aag cca ggc acc att cgt ggg gac ttc tgc   399
194 Thr Asn Pro Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys
195      95              100              105
197 att cag gtt ggc agg aac atc att cat ggc agt gat tca gta aaa agt   447
198 Ile Gln Val Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser
199 110              115              120              125
201 gct gaa aaa gaa atc agc cta tgg ttt aag cct gaa gaa ctg gtt gac   495
202 Ala Glu Lys Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp
203              130              135              140
205 tac aag tct tgt gct cat gac tgg gtc tat gaa taagaggtgg acacaacagc  548
206 Tyr Lys Ser Cys Ala His Asp Trp Val Tyr Glu
207              145              150
209 agtctccttc agcacggcgt ggtgtgtccc tggacacagc tcttcattcc attgacttag  608
210 aggcaacagg attgatcatt cttttataga gcatatttgc caataaagct tttggaagcc  668
211 gg                                                                670
213 <210> SEQ ID NO: 5
214 <211> LENGTH: 152
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 5
219 Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val
220  1               5               10               15
221 Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly
222              20               25               30
223 Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu
224          35               40               45
225 Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu
226      50               55               60
227 Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly
228 65               70               75               80
229 Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro
230              85               90               95
231 Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val
232          100              105              110
233 Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys
234          115              120              125
235 Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp Tyr Lys Ser
```

RAW SEQUENCE LISTING   DATE: 07/05/2005
PATENT APPLICATION: **US/10/074,694**   TIME: 14:27:54

Input Set : **A:\10276-017002.TXT**
Output Set: **N:\CRF4\07052005\J074694.raw**

```
236     130                  135                140
237 Cys Ala His Asp Trp Val Tyr Glu
238 145                 150
```

VERIFICATION SUMMARY   DATE: 07/05/2005
PATENT APPLICATION: **US/10/074,694** TIME: 14:27:55

Input Set : **A:\10276-017002.TXT**
Output Set: **N:\CRF4\07052005\J074694.raw**